

STIC-Biotech/ChemLib

129776

From: Winkler, Ulrike  
Sent: Thursday, August 12, 2004 11:42 AM  
To: STIC-Biotech/ChemLib

STIC

Please do a sequence alignment between the following sequences

SEQ ID NO: 1 of US Pat No. 5942607 and SEQ ID NO: 5 of application # 09/303510

and

SEQ ID NO: 2 of US Pat No. 5942607 and SEQ ID NO: 6 of application # 09/303510

CRFE

Thanks, Ulrike

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(103)

Freeman is human CD80  
CD86

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STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

IntelliGenetics

# PaasDB - Fast Pairwise Comparison of Sequences

## Release 5.4

Results file 5942607-1\_x\_303510-5.res made by spaula on Tue 17 Aug 104 16:38:38-PST.

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Query sequence being compared: US-08-101-624-1 (1-1120)
Number of sequences searched: 1
Number of scores above cutoff: 1
```



> O < Intelligenetics  
> O <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 5942607-2\_x\_303510-6.res made by epaula on Tue 17 Aug 104 16:36:51-EST.

Query sequence being compared: US-08-101-624-2 (1-329)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-08-101-624-2 (1-329) with:  
File : US09303510Amod.pep

100-  
N -  
U 50-  
M -  
B -  
E -  
R -  
O -  
F 10-  
S -  
E 5-  
U -  
N -  
E -  
N -  
C -  
E -  
S 0-  
SCORE 0 13 25 38 51 63 76 89 101 114  
STDEV

## PARAMETERS

Similarity matrix Unitary 1 K-tuple 2  
Mismatch penalty 1.00 Joining penalty 20  
Gap penalty 0.05 Window size 329  
Cutoff score 0  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean 114 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 329  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt. Sig. Frame				
1. US-08-101-624-2 (1-329)	US-09-303-510-6 Sequence 6, Application US	329	114	184 0.00 0				
Initial Score = 114 Optimized Score = 184 Significance = 0.00								
Residue Identity = 57% Matches = 192 Mismatches = 130								
Gaps = 10 Conservative Substitutions = 0								
X	MDPQCTMGISNIIIFVMAFLISGAAPLKIQAIFNETADLPQCFANSONOSLSSELYVFMODQENLVINEVYLG	10	20	30	40	50	60	70
X	MGICDSTWGLSHTLLVMAFLISGVSSMKSQAYFNTGELPCHFTNSONISLDELVFMWODQKLVLYEIRFG	10	20	30	40	50	60	70
X	KEKPSVHAKYMGRTSPDSWTLRLHNIQIKDKGLYOCIIHKKKPTGKIRIHONKSELSVLANFSQPEIVP	80	90	100	110	120	130	140
X	KENPQVHLKYGKRTSPDKDNTLRLHNVQIKDKGYHCFIHYKGPKGIVPMHOMSSDLSVLANSQPEITV	80	90	100	110	120	130	140
X	ISNITBN-VYINLTGSSIHGYPEPKMSVLTFTKNGSTIEYDGIQKSDQNTVELYDVISLSVSFPDVTSM	150	160	170	180	190	200	210
X	TSNRTENSGIIMLTGSSIOGYPEPKEMFOLNTENSTTKYDVMKKSQNNVTLEYVNSISLPSVP-EAHNV	150	160	170	180	190	200	210
X	TIFC--ILETDKTRLLSSPFSI--ELEDPQPPDHI PWITAVL-PTVITICVAVFCLIIKKMKKKRPRNSYK	220	230	240	250	260	270	280
X	SVFCALKLET-LEMILSLPFINIDAPKDKDPEQGHFLWIAVLVAFVFCGAVSFKTLRK-RKKQPGPSHE	220	230	240	250	260	270	280
X	CCTNTERESESQTKREKIHIPERSDEAQRVFKSKTSKTSKSPDTCF	290	300	310	320	330	340	350
X	CETIKRERKESKQTERVYVHYVPERSEDAQCV-NILKTPASGDKNQ	290	300	310	320	330	340	350